



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Morris Reichlin and Eugen Koren
- (ii) TITLE OF INVENTION: METHOD FOR TREATMENT OF SLE

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

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1201 West Peachtree Street
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/800,682
- (B) FILING DATE: 14-FEB-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US96/07597
- (B) FILING DATE: 24-MAY-1996
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/011,867
- (B) FILING DATE: 15-FEB-1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Pabst, Patrea L.
- (B) REGISTRATION NUMBER: 31,284
- (C) REFERENCE/DOCKET NUMBER: OMRF 158 CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

GGTGAAGAAG GAGTTGTGCC AGCACGTGAG TACTCAGACG ATCGTAACAT CAACCTGGCA	60
GACGAATTAA AAATTGGTGA TACCATTGAA GCAGTTGTCA TTTCTAACGT AACAAGCGAC	120
AAGGAAGGCG TCAGTTACTT GTTGTCAAAG AAGCGTTTGG ATGCGCGCAA GGCATGGGAA	180
AACTTGAGCT TTGCTGAAGG TGACACAGTT GATGCCAAGG TTATCAACGC TGTTCGTGGT	240
GGTTTGATTG TTGATGTTAA CGGCGTACGT GGTTCGTAC CAGCATCAAT GGTTGCAGAA	300
CGTTTCGTTT CTGATTTGAA CCAATTCAAG AATAAGGATA TTAAAGCACA AGTTATCGAA	360
ATTGACCCTG CTAATGCACG TTTGATTTTG TCACGTAAGG CTGTTGCTGC ACAAGAACGC	420
GCTGCACGAT TGGCTGAAGT ATTTAGCAAG TTGTCAGTTC GTGAAGTTGT TGAAGGAACT	480
GTTGCCCGTT TGACAGACTT CGGCGCATTG GTTGACTTGG GTGGTGTGA TGGTTTGGTT	540
CACGTATCAG AAATCTCACA CGATCGTGTG AAGAACCCGG CCGATGTATT GACAAAGGGT	600
GACAAGGTTG ATGTTAAGAT CTTGGCATTG GACACTGAAA AGGGTCGTAT CTCATTGTCA	660
ATCAAAGCAA CACAACGTGG ACCTTGGGAC GAAGCTGCAG ATCAAATCGC TGCAGGTTCA	720
GTGCTTGAAG GTACTGTTAA GCGTGTGAAG GACTTTGGTG CCTTTGTTGA AATTTTGCCT	780
GGTATCGAAG GTCTTGTGCA CGTGTCAACA ATTTCAAACA AGCGTATTGA AAACCCATCA	840
GAAGTTTTGA AGTCTGGTGA CAAGGTACAA GTGAAGGTAT TGGACATTAA GCCAGCCGAA	900
GAACGTATTT CATTGTCAAT GAAGGCTTTG GAAGAAAAGC CAGAACGTGA AGATCGTCGT	960
GGTAACGATG GTTCAGCTTC ACGTGCTGAT ATCGCTGCTT ACAAGCAACA AGATGACTCA	1020
CCCACAACAT TGGGTGACAT CTTTGGTGAT AAGTTGTAAG AGGCATCAAC ATAAAAGAGC	1080
TGGTTCGCCA GTTCTTTTAT TTTTGAAGAA AAATTGAGTG GGCATTAGTG GCGCTCACG	1140
GTATGAAAAA GGAGGTGCGA TTATGGCAGC ACCAGTAGTA GCCATTGTTG GCGACCAAAC	1200
GTCGGAATAT CGACTATCTT TAACCGGATG GCCGGAGAAC GTATTGCAAT TGTTGAAGAT	1260
CAACCAGGGG TAACACGCGA TCGTTTGTAC GCGCCAGCCG AATGGTTGAA TTAT	1314

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 352 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg Asn

1	5	10	15
Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu Ala Val	20	25	30
Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser Tyr Leu Leu	35	40	45
Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu Asn Leu Ser Phe	50	55	60
Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val Arg Gly	65	70	75
Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro Ala Ser	85	90	95
Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys Asn Lys	100	105	110
Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala Arg Leu	115	120	125
Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala Gln Leu	130	135	140
Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu Gly Thr	145	150	155
Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val	165	170	175
Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn	180	185	190
Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu	195	200	205
Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr	210	215	220
Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser	225	230	235
Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe Val	245	250	255
Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln Ile Ser	260	265	270
Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly Asp Lys	275	280	285
Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg Ile Ser	290	295	300
Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu Asp Arg Arg			

305                      310                      315                      320  
 Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp Ile Ala Ala Tyr Lys Gln  
                                  325                                   330                                   335

Gln Asp Asp Ser Ala Ala Thr Leu Gly Asp Ile Phe Gly Asp Lys Leu  
                                  340                                   345                                   350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val  
 1                                      5                                      10                                      15

Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro  
                                  20                                      25                                      30

Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys  
                                  35                                      40                                      45

Asn Lys Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala  
                                  50                                      55                                      60

Arg Leu Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala  
 65                                      70                                      75                                      80

Gln Leu Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu  
                                  85                                      90                                      95

Gly Thr Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly  
                                  100                                      105                                      110

Gly Val Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val  
                                  115                                      120                                      125

Lys Asn Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys  
                                  130                                      135                                      140

Ile Leu Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys  
 145                                      150                                      155                                      160

Ala Thr Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala  
                                  165                                      170                                      175

Gly Ser Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala  
                                  180                                      185                                      190

Phe Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln  
                                  195                                      200                                      205

Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly  
 210 215 220

Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg  
 225 230 235 240

Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu  
 245 250 255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Ala Tyr Glu Asp Ala Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val  
 1 5 10 15

Lys Gly Gly Phe Thr Val Glu Leu Asp Gly Ile Arg Ala Phe Leu Pro  
 20 25 30

Gly Ser Leu Val Asp Val Arg Pro Val Arg Asp Thr Leu His Leu Glu  
 35 40 45

Gly Lys Glu Leu Glu Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn  
 50 55 60

Asn Val Val Val Ser Arg Arg Ala Val Ile Glu Ser Glu Asn Ser Ala  
 65 70 75 80

Glu Arg Asp Gln Leu Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys  
 85 90 95

Gly Ile Val Lys Asn Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly  
 100 105 110

Gly Val Asp Gly Leu Leu His Ile Thr Asp Met Ala Trp Lys Arg Val  
 115 120 125

Lys His Pro Ser Glu Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys  
 130 135 140

Val Leu Lys Phe Asp Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys  
 145 150 155 160

Gln Leu Gly Glu Asp Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu  
 165 170 175

Gly Thr Lys Leu Thr Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys  
 180 185 190

Phe Val Glu Ile Glu Glu Gly Val Glu Gly Leu Val His Val Ser Glu  
 195 200 205  
 Met Arg Asp Arg Val Glu Asp Ala Thr Leu Val Leu Ser Val Gly Asp  
 210 215 220  
 Glu Val Glu Ala Lys Phe Thr Gly Val Asp Arg Lys Asn Arg Ala Ile  
 225 230 235 240  
 Ser Leu Ser Val Arg Ala Lys Asp Glu Ala Asp Glu Lys Asp  
 245 250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Lys Phe Glu Ala Gly Glu Arg Val Glu Gly Ile Ile Phe Asn Gln Val  
 1 5 10 15  
 Lys Gly Gly Phe Thr Val Asp Leu Asp Gly Ala Val Ala Phe Leu Pro  
 20 25 30  
 Arg Ser Gln Val Asp Ile Arg Pro Ile Arg Asp Val Thr Pro Ala Asp  
 35 40 45  
 Ala Gln Pro Ala Ala Leu Arg Asn Leu Lys Met Asp Lys Arg Arg Gly  
 50 55 60  
 Asn Ile Val Val Ser Arg Arg Thr Val Leu Glu Glu Ser Arg Ala Glu  
 65 70 75 80  
 Gln Arg Ser Glu Ile Val Gln Asn Leu Glu Glu Gly Gln Val Val Glu  
 85 90 95  
 Gly Val Val Lys Asn Ile Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly  
 100 105 110  
 Gly Ile Asp Gly Leu Leu His Val Thr Asp Met Ala Trp Arg Arg Val  
 115 120 125  
 Lys His Pro Ser Glu Ile Gln Asn Ile Gly Gln Gln Val Lys Val Gln  
 130 135 140  
 Ile Ile Arg Ile Asn Gln Glu Thr His Arg Ile Ser Leu Gly Met Lys  
 145 150 155 160  
 Gln Leu Glu Ser Asp Pro Trp Asp Gly Ile Gly Ala Lys Tyr Pro Val  
 165 170 175

Gly Lys Lys Ile Ser Gly Thr Val Thr Asn Ile Thr Asp Tyr Gly Ala  
180 185 190

Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Glu  
195 200 205

Met Asn Arg Pro Gly Glu Gln Val Ile Glu Glu Phe Asn Lys Gly Asp  
210 215 220

Val Val Arg Ala Val Val Leu Asp Val Asp Val Asp Lys Glu Arg Ile  
225 230 235 240

Ser Leu Gly Ile Lys Gln Leu  
245

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val Lys Gly Gly Phe Thr  
1 5 10 15

Val Glu Leu Asn Gly Ile Arg Ala Phe Leu Pro Gly Ser Leu Val Asp  
20 25 30

Val Arg Pro Val Arg Asp Thr Thr His Leu Glu Gly Lys Glu Leu Glu  
35 40 45

Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn Asn Val Val Val Ser  
50 55 60

Arg Arg Ala Val Ile Glu Ser Glu Ser Ser Ala Glu Arg Asp Gln Leu  
65 70 75 80

Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys Gly Ile Val Lys Asn  
85 90 95

Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu  
100 105 110

Leu His Ile Thr Asp Met Ala Trp Lys Arg Val Lys His Pro Ser Glu  
115 120 125

Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys Val Leu Lys Phe Asp  
130 135 140

Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys Gln Leu Gly Glu Asp  
145 150 155 160

Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu Gly Thr Lys Leu Thr  
165 170 175

Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys Phe Val Glu Ile Glu  
180 185 190

Glu Gly Val Glu Gly Leu Val His Val Ser Glu Met Lys Lys Gly Asp  
195 200 205

Glu Ile Ala Ala Val Val Leu Gln Val Asp Ala Glu Arg Glu Arg Ile  
210 215 220

Ser Leu Gly Val Lys Gln Leu Ala Glu Asp Pro  
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Ala Glu Asp Val Val Val Lys Gly Lys Ile Val Gly Ala Asn Lys Gly  
1 5 10 15

Gly Val Val Ala Leu Val Glu Gly Leu Arg Gly Phe Val Pro Phe Ser  
20 25 30

Gln Ile Ser Ser Lys Ser Ser Ala Glu Glu Leu Leu Glu Lys Glu Ile  
35 40 45

Pro Leu Lys Phe Val Glu Val Asp Glu Glu Gln Ser Arg Leu Val Met  
50 55 60

Ser Asn Arg Lys Ala Met Ala Asp Ser Gln Ala Met Ala Asp Ser Gln  
65 70 75 80

Ala Gln Leu Gly Ile Gly Ser Val Val Thr Gly Thr Val Gln Ser Leu  
85 90 95

Lys Pro Tyr Gly Ala Phe Ile Asp Ile Gly Gly Ile Asn Gly Leu Leu  
100 105 110

His Val Ser Gln Ile Ser His Asp Arg Val Ser Asp Ile Ala Thr Val  
115 120 125

Leu Gln Pro Gly Asp Thr Leu Lys Val Met Ile Leu Ser His Asp Arg  
130 135 140

Glu Arg Gly Arg Val Ser Leu Ser Thr Lys Lys Leu Glu Pro Thr Pro  
145 150 155 160



Gly Asp

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Gly Thr Val

1

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Asp Phe Gly Ala Phe Val

1

5

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Gly Leu Val His Val Ser

1

5

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Gly Asp Lys Val

1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Arg Ile Ser Leu Ser

1

5